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## RAW SEQUENCE LISTING

DATE: 08/30/2004

PATENT APPLICATION: US/10/762,665

TIME: 14:41:34

Input Set : N:\Crf3\RULE60\10762665.raw.txt

Output Set: N:\CRF4\08302004\J762665.raw

1 <110> APPLICANT: Fuchs, Renate  
 2 Wilske, Bettina  
 3 Motz, Manfred  
 4 Soutscheck, Erwin  
 5 Preeac-Mursic, Vera  
 6 <120> TITLE OF INVENTION: Active proteins from Borrelia  
 7 burgdorferi  
 8 <130> FILE REFERENCE: 738.001US3  
 9 <140> CURRENT APPLICATION NUMBER: US/10/762,665  
 10 <141> CURRENT FILING DATE: 2004-01-22  
 11 <150> PRIOR APPLICATION NUMBER: US/09/711,546  
 12 <151> PRIOR FILING DATE: 2000-11-13  
 13 <150> PRIOR APPLICATION NUMBER: US 09/196,293  
 14 <151> PRIOR FILING DATE: 1998-11-19  
 15 <150> PRIOR APPLICATION NUMBER: US 08/209,603  
 16 <151> PRIOR FILING DATE: 1994-03-10  
 17 <150> PRIOR APPLICATION NUMBER: US 07/862,535  
 18 <151> PRIOR FILING DATE: 1992-06-19  
 19 <150> PRIOR APPLICATION NUMBER: WO PCT/EP90/02282  
 20 <151> PRIOR FILING DATE: 1990-12-21  
 21 <150> PRIOR APPLICATION NUMBER: DE P40 18 988.0  
 22 <151> PRIOR FILING DATE: 1990-06-13  
 23 <150> PRIOR APPLICATION NUMBER: DE P39 42 728.5  
 24 <151> PRIOR FILING DATE: 1989-12-22  
 25 <160> NUMBER OF SEQ ID NOS: 16  
 26 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 28 <210> SEQ ID NO: 1  
 29 <211> LENGTH: 39  
 30 <212> TYPE: DNA  
 31 <213> ORGANISM: Borrelia burgdorferi  
 32 <400> SEQUENCE: 1  
 33 atgaccatga ttacgaattc ccggggatcc atcatgatt  
 35 <210> SEQ ID NO: 2  
 36 <211> LENGTH: 20  
 37 <212> TYPE: PRT  
 38 <213> ORGANISM: Borrelia burgdorferi  
 39 <400> SEQUENCE: 2  
 40 Glu Leu Asp Lys Glu Lys Leu Lys Asp Phe Val Asn Leu Asp Leu Glu  
 41 1 5 10 15  
 42 Phe Val Asn Thr  
 43 20  
 45 <210> SEQ ID NO: 3  
 46 <211> LENGTH: 61

39

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47 <212> TYPE: DNA
48 <213> ORGANISM: Borrelia burgdorferi
49 <400> SEQUENCE: 3
50 garytdgaya argaraaryt daargaytty gtwaayytdg ayyadgartt ygtwaaytay 60
51 a 61
53 <210> SEQ ID NO: 4
54 <211> LENGTH: 346
55 <212> TYPE: DNA
56 <213> ORGANISM: Borrelia burgdorferi
57 <400> SEQUENCE: 4
58 atgaaaaaaa tgttactaat ctttagtttt tttcttgttt ttttaaattg atttcctctt 60
59 aatgcaaggg aagttgataa ggaaaaatta aaggactttg ttaatatgga tcttgaattt 120
60 gttaattaca agggtcctta tgattctaca aatacatatg aacaaatagt aggtattggg 180
61 gagtttttag caaggccgtt gatcaattcc aatagtaagt caagttatta tggtaaatat 240
62 tttgttaata gatttattga cgatcaagat aaaaaagcaa gtgttgatat tttttctatt 300
63 ggtagtaagt cagagcttga tagtatatta aatctaagaa gaattc 346
65 <210> SEQ ID NO: 5
66 <211> LENGTH: 663
67 <212> TYPE: PRT
68 <213> ORGANISM: Borrelia burgdorferi
69 <400> SEQUENCE: 5
70 Met Lys Lys Met Leu Leu Ile Phe Ser Phe Phe Leu Val Phe Leu Asn
71 1 5 10 15
72 Gly Phe Pro Leu Asn Ala Arg Glu Val Asp Lys Glu Lys Leu Lys Asp
73 20 25 30
74 Phe Val Asn Met Asp Leu Glu Phe Val Asn Tyr Lys Gly Pro Tyr Asp
75 35 40 45
76 Ser Thr Asn Thr Tyr Glu Gln Ile Val Gly Ile Gly Glu Phe Leu Ala
77 50 55 60
78 Arg Pro Leu Ile Asn Ser Asn Ser Ser Tyr Tyr Gly Lys Tyr
79 65 70 75 80
80 Phe Val Asn Arg Phe Ile Asp Asp Gln Asp Lys Lys Ala Ser Val Asp
81 85 90 95
82 Ile Phe Ser Ile Gly Ser Lys Ser Glu Leu Asp Ser Ile Leu Asn Leu
83 100 105 110
84 Arg Arg Ile Leu Thr Gly Tyr Leu Ile Lys Ser Phe Asp Tyr Glu Arg
85 115 120 125
86 Ser Ser Ala Glu Leu Ile Ala Lys Ala Ile Thr Ile Tyr Asn Ala Val
87 130 135 140
88 Tyr Arg Gly Asp Leu Asp Tyr Tyr Lys Glu Phe Tyr Ile Glu Ala Ser
89 145 150 155 160
90 Leu Lys Ser Leu Thr Lys Glu Asn Ala Gly Leu Ser Arg Val Tyr Ser
91 165 170 175
92 Gln Trp Ala Gly Lys Thr Gln Ile Phe Ile Pro Leu Lys Lys Asn Ile
93 180 185 190
94 Leu Ser Gly Asn Val Glu Ser Asp Ile Asp Ile Asp Ser Leu Val Thr
95 195 200 205
96 Asp Lys Val Val Ala Ala Leu Leu Ser Glu Asn Glu Ser Gly Val Asn
97 210 215 220

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98 Phe Ala Arg Asp Ile Thr Asp Ile Gln Gly Glu Thr His Lys Ala Asp
99 225 230 235 240
100 Gln Asp Lys Ile Asp Ile Glu Leu Asp Asn Phe His Glu Ser Asp Ser
101 245 250 255
102 Asn Ile Thr Glu Thr Ile Glu Asn Leu Arg Asp Gln Leu Glu Lys Ala
103 260 265 270
104 Thr Asp Glu Glu His Lys Lys Glu Ile Glu Ser Gln Val Asp Ala Lys
105 275 280 285
106 Lys Lys Gln Lys Glu Glu Leu Asp Lys Lys Ala Ile Asp Leu Asp Lys
107 290 295 300
108 Ala Gln Gln Lys Leu Asp Phe Ala Glu Asp Asn Leu Asp Ile Gln Arg
109 305 310 315 320
110 Asp Thr Val Arg Glu Lys Leu Gln Glu Asn Ile Asn Glu Thr Asn Lys
111 325 330 335
112 Glu Lys Asn Leu Pro Lys Pro Gly Asp Val Ser Ser Pro Lys Val Asp
113 340 345 350
114 Lys Gln Leu Gln Ile Lys Glu Ser Leu Glu Asp Leu Gln Glu Gln Leu
115 355 360 365
116 Lys Glu Ala Ser Asp Glu Asn Gln Lys Arg Glu Ile Glu Lys Gln Ile
117 370 375 380
118 Glu Ile Lys Lys Asn Asp Glu Glu Leu Phe Lys Asn Lys Asp His Lys
119 385 390 395 400
120 Ala Leu Asp Leu Lys Gln Glu Leu Asn Ser Lys Ala Ser Ser Lys Glu
121 405 410 415
122 Lys Ile Glu Gly Glu Glu Glu Asp Lys Glu Leu Asp Ser Lys Lys Asn
123 420 425 430
124 Leu Glu Pro Val Ser Glu Ala Asp Lys Val Asp Lys Ile Ser Lys Ser
125 435 440 445
126 Asn Asn Asn Glu Val Ser Lys Leu Ser Pro Leu Asp Glu Pro Ser Tyr
127 450 455 460
128 Ser Asp Ile Asp Ser Lys Glu Gly Val Asp Asn Lys Asp Val Asp Leu
129 465 470 475 480
130 Gln Lys Thr Lys Pro Gln Val Glu Ser Gln Pro Thr Ser Leu Asn Glu
131 485 490 495
132 Asp Leu Ile Asp Val Ser Ile Asp Ser Ser Asn Pro Val Phe Leu Glu
133 500 505 510
134 Val Ile Asp Pro Ile Thr Asn Leu Gly Thr Leu Gln Leu Ile Asp Leu
135 515 520 525
136 Asn Thr Gly Val Arg Leu Lys Glu Ser Ala Gln Gln Gly Ile Gln Arg
137 530 535 540
138 Tyr Gly Ile Tyr Glu Arg Glu Lys Asp Leu Val Val Ile Lys Ile Asp
139 545 550 555 560
140 Ser Gly Lys Ala Lys Leu Gln Ile Leu Asp Lys Leu Glu Asn Leu Lys
141 565 570 575
142 Val Ile Ser Glu Ser Asn Phe Glu Ile Asn Lys Asn Ser Ser Leu Tyr
143 580 585 590
144 Val Asp Ser Arg Met Ile Leu Val Val Lys Asp Asp Ser Asn Ala
145 595 600 605
146 Trp Arg Leu Ala Lys Phe Ser Pro Lys Asn Leu Asp Glu Phe Ile Leu

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```

147          610          615          620
148 Ser Glu Asn Lys Ile Leu Pro Phe Thr Ser Phe Ala Val Arg Lys Asn
149 625          630          635          640
150 Phe Ile Tyr Leu Gln Asp Glu Leu Lys Ser Leu Val Thr Leu Asp Val
151          645          650          655
152 Asn Thr Leu Lys Lys Val Lys
153          660
155 <210> SEQ ID NO: 6
156 <211> LENGTH: 13
157 <212> TYPE: PRT
158 <213> ORGANISM: Borrelia burgdorferi
159 <400> SEQUENCE: 6
160 Lys Ile Thr Asp Ser Asn Ala Thr Val Leu Ala Val Lys
161 1          5          10
163 <210> SEQ ID NO: 7
164 <211> LENGTH: 11
165 <212> TYPE: PRT
166 <213> ORGANISM: Borrelia burgdorferi
167 <400> SEQUENCE: 7
168 Asp Leu Phe Glu Ser Val Glu Gly Leu Leu Lys
169 1          5          10
171 <210> SEQ ID NO: 8
172 <211> LENGTH: 40
173 <212> TYPE: DNA
174 <213> ORGANISM: Borrelia burgdorferi
175 <400> SEQUENCE: 8
176 aaratwacwg aywcwaaygc wacwgtwytd gcwgtwaara 40
178 <210> SEQ ID NO: 9
179 <211> LENGTH: 34
180 <212> TYPE: DNA
181 <213> ORGANISM: Borrelia burgdorferi
182 <400> SEQUENCE: 9
183 gayytdttyg arwcwgtwga rgghytdytd aara 34
185 <210> SEQ ID NO: 10
186 <211> LENGTH: 639
187 <212> TYPE: DNA
188 <213> ORGANISM: Borrelia burgdorferi
189 <400> SEQUENCE: 10
190 atgaaaaaga atacattaag tgcgatatta atgactttat ttttatttat atcttgtaat 60
191 aattcaggga aggtggggat tctgcatcta ctaatcctgc tgacgagtct tgcgaaaggg 120
192 cctaactcta cagaaataag caaaaaaatt acagattcta atgcatttgt acttgctggt 180
193 aaagaagttg agactttggt tttatctata gatgaacttg ctaagaaagc tattgggtcaa 240
194 aaaatagaca ataataatgg tttagctgct ttaaataatc agaatggatc gttgtagaca 300
195 ggagcctatg caatatcaac cctaataaca gaaaaattga gtaaattgaa aaatttagaa 360
196 gaattaaaga cagaaattgc aaaggctaag aaatgttccg aagaatttac taataaacta 420
197 aaaagtggtc atgcagatct tggcaaacag gatgctaccg atgatcatgc aaaagcagct 480
198 attttaaaaa cacatgcaac taccgataaa ggtgctaaag aatttaaaga tttatttgaa 540
199 tcagtagaag gtttggttaa agcagctcaa gtagcactaa ctaattcagt taaagaactt 600
200 acaagtcctg ttgtagcaga aagtccaaaa aaaccttaa 639

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Input Set : N:\Crif3\RULE60\10762665.raw.txt

Output Set: N:\CRF4\08302004\J762665.raw

202 &lt;210&gt; SEQ ID NO: 11

203 &lt;211&gt; LENGTH: 212

204 &lt;212&gt; TYPE: PRT

205 <213> ORGANISM: *Borrelia burgdorferi*

206 &lt;400&gt; SEQUENCE: 11

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207 Met Lys Lys Asn Thr Leu Thr Ala Ile Leu Met Thr Leu Phe Leu Phe
208      1              5              10              15
209 Ile Ser Cys Asn Asn Ser Gly Lys Val Gly Ile Leu Thr Ser Thr Asn
210      20              25              30
211 Pro Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
212      35              40              45
213 Lys Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu
214      50              55              60
215 Thr Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln
216      65              70              75              80
217 Lys Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly
218      85              90              95
219 Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys
220      100             105             110
221 Leu Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys
222      115             120             125
223 Ala Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His
224      130             135             140
225 Ala Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala
226      145             150             155             160
227 Ile Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys
228      165             170             175
229 Asp Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala
230      180             185             190
231 Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser
232      195             200             205
233 Pro Lys Lys Pro
234      210

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236 &lt;210&gt; SEQ ID NO: 12

237 &lt;211&gt; LENGTH: 680

238 &lt;212&gt; TYPE: DNA

239 <213> ORGANISM: *Borrelia burgdorferi*

240 &lt;400&gt; SEQUENCE: 12

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241 atgaaaaaat atttattggg aataggtcta atattagcct taatagcatg caagcaaaat      60
242 gtttagcagcc ttgatgaaaa aaacagcgct tcagtagatt tgcctggtga gatgaaagtt      120
243 cttgtaagta aagaaaaaga caaagacggt aagtacagtc taaaggcaac agtagacaag      180
244 attgagctaa aaggaaacttc tgataaagac aatggttctg gggtgcttga aggtacaaaa      240
245 gatgacaaaa gtaaagcaaa attaacaatt gctgacgatc taagtaaaac cacattcgaa      300
246 cttttcaaag aagatggcaa aacattagtg tcaagaaaag taagttctaa agacaaaaca      360
247 tcaacagatg aaatgttcaa tgaaaaagggt gaattgtctg caaaaacccat gacaagagaa      420
248 aatggaacca aacttgaata tacagaaatg aaaagcgatg gaaccggaaa agctaaagaa      480
249 gttttaaaaa actttactct tgaaggaaaa gtagctaatt ataaagtaac attggaagta      540
250 aaagaaggaa ccgttacttt aagtaaggaa attgcaaaat ctggagaagt aacagttgct      600
251 cttaatgaca ctaacactac tcaggctact aaaaaaactg gcgcatggga ttcaaaaact      660

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**VERIFICATION SUMMARY**

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